Estimation of breeding values of Belgian Black and White, Red and White, White Red and Red of Flanders breeds with the animal model.

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Introduction

In Belgium, since 1978, sire evaluations were based on quantitative and qualitative first lactation records using a sire model including group of origin, age of calving, current calving interval and herd level - year - season class.

Due to import of semen especially from USA and Canada, genetic groups corresponding to Holstein genes % were considered. Besides the estimation of breeding values, a net economic merit index (INET) including Milk, Fat and Protein has been developped (Volckaert 1988) and linear programming techniques were used to maximize profit (the INET) when choosing dairy bulls (Leroy and Farnir 1990).

Since 1987, the animal model (AM) allowing simultaneous evaluation of sires an cows has been studied in the belgian black and white breed in order to inform the people in charge of selection on the new methodology and in order to establish the best computing strategy for the global material. (Leroy and VanVleck (1987), Leroy and Farnir (1990)).

In 1993 the fisrt national AM evaluation in Belgium was scheduled and the results are presented hereafter.

Material and methods

Data

First, second and third lactations of cows with parents known or unknown belonging to Belgian Black and White, Red and White, White Red and Red of Flanders breeds were obtained from the Vlaamse Rundveeteelt Vereniging (VRV) and the Ministry of Agriculture.

Extrapolated 305-d productions from partial lactation ≥ 100 days and 305-d complete records were obtained for milk, fat and protein quantitative productions. The data were not precorrected for non genetic factors.

All the pedigrees were traced as far as the information was available starting with the informations obtained from the different exporting countries present in Belgium. When parents were not found virtual parents were created and put in genetic groups according to the information known (country of origin of sire when known, year of birth of the cow). The methodology applied was similar to the grouping strategy of Westell (1984) and Quaas (1988).

Model

The data were analysed with the folowing linear model:

$$Y_{ijklmn} = mg_i + age_j + cc_k + m_l + u_m + p_m + e_{mn}$$

where

Y_{ijklmn}	=	milk, fat, protein (Kg) 1st, 2nd, 3rd lactation 305-d record.
mg_i	=	fixed management group effect
age_j	=	fixed age effect (all lactations)
cc_k	=	fixed current calving interval effect
m_l	=	fixed month of calving effect
u_m	=	random additive genetic effect (a) + group (g)
p_m	=	random permanent environment effect
e_{ijkmn}	=	random residual effect

in matrix notation:

$$y = Xb + Zu + Zp + e$$

where

X,Z are the coresponding incidence matrices.

b is the vector corresponding to all fixed effects, u to the additive genetic + group effects

and p to the permanent environmental effect.

and

$$E(y) = Xb + ZQg$$
$$E(u) = ZQg.$$

Where Q is a matrix having rows (number of rows = size of the vector animals) indicating the proportion of each group of unknown parents in the genotype of the animal. The model is to be compared with the models developed by Westell (1984), Westell and VanVleck (1987), Leroy and Farnir (1990).

Computing strategy

Permanent environmental effect was eliminated by absorption.

The equation system has been divided in four main parts:

-the age,season and calving interval fixed effects part

-the management group fixed effects part

-the cow part

-the sire and group part

This strategy allows parallel computing which will be implemented later and especially the iteration in cow and management group equations in slaves cpu directly connected with a master cpu where the iteration process concern sires, groups and other non genetic effects (except management groups) common to the other equations (cows, management groups) and where previous sire, group and non genetic effects solutions are available for each slave (figure 1). The gain obtained in a previous study was 1.48 with 2 processors and 2.99 with 4 processors (Leroy and Farnir 1990).

Iteration was done on the data or in core (for breeds with ≤500,000 records). Convergence was measured by the relative squared diffrence between consecutive rounds.

Figure 1. Parallel computing with the animal model in dairy cattle.

Cows
Management groups

Fixed effects (age, season,cci)

Sires and groups
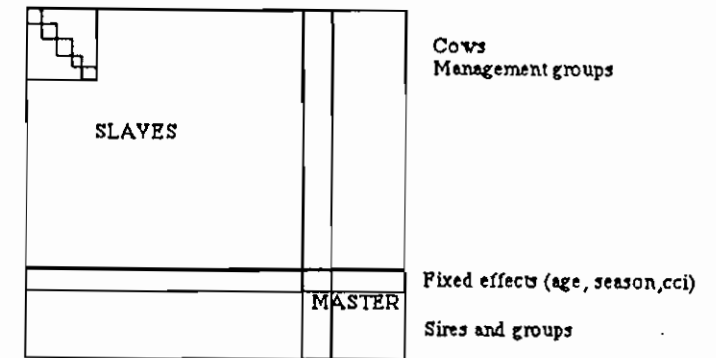
Results and discussion

The sire solutions were compared with previous estimations obtained with a sire model. Correlations between the two evaluation procedures are given in table 1 for the 4 breeds. The corresponding figure for the Black and White breed is given in figure 2.

Table 1. Correlations between Blup sire model and Animal Model in the four belgian dairy breeds.

	Milk kilo	Fat kilo	Protein kilo	Fat%	Prot.%
Black an White	0.81546	0.74276	0.77443	0.90104	0.87565
Red and White	0.90893	0.85242	0.80427	0.76647	0.60017
White Red	0.95043	0.95812	0.91400	0.96774	0.84155
Red of Flanders	0.60133	0.55043	0.48141	0.40061	0.51495
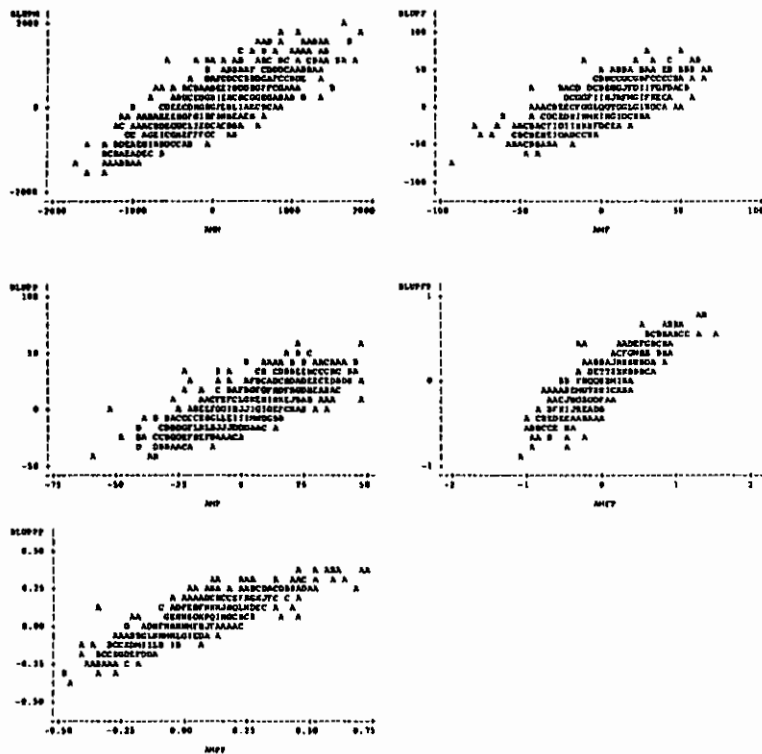
The cow solutions are presented in table 2 for the Red of Flanders breed and the estimated genetic trend is given in figure 3 for the same breed.

Due to the good relation with the previous system, the joint evaluation of sires and cows with the animal model has been well accepted and has been generalized in Belgium in 1993.
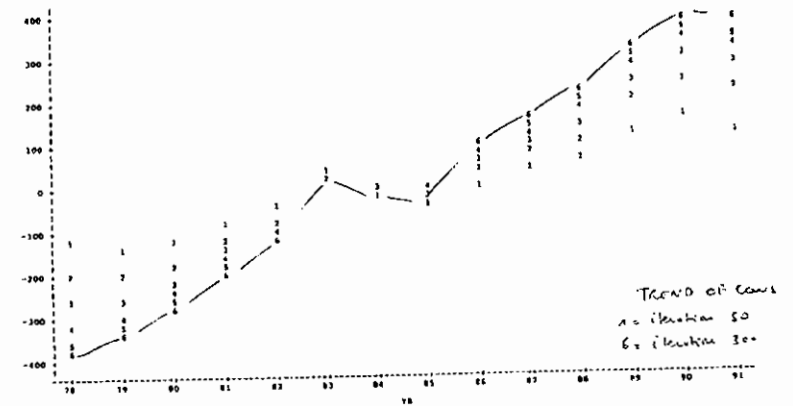
Estimation of breeding values for somatic cell counts will be included soon and will be the first non production trait evaluated in Belgium.

Further work will concern the parallel computing approach, the incorporation of foreign data, the introduction of daughter yield deviations in the international evaluation program developed by Interbull and the estimation of breeding values for type traits.

Table 2. Estimated breed values in the Red of Flanders breed (by bith year).

YB	N Obs	N	Mean	Std Dev
78	2430	2430	-314.365	243.367
79	2485	2485	-294.437	224.421
80	2706	2706	-242.874	252.491
81	2825	2825	-165.640	305.424
82	2902	2902	-98.920	306.175
83	3063	3063	19.940	342.333
84	2769	2769	0.208	361.862
85	2371	2371	-7.022	354.280
86	2427	2427	70.174	348.486
87	2296	2296	122.706	363.225
88	2234	2234	172.553	378.501
89	2250	2250	277.800	407.787
90	1804	1804	336.216	380.926
91	218	218	312.872	352.675

Figure 3. Estimated genetic trend according to iteration number in the Red of Flanders Breed.(1=iteration 50, 6=iteration 300).

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